IN THE SPECIFICATION

Please replace the paragraph beginning at page 3, line 13 with the following amended paragraph:

The two known forms of lysozymes, chicken-type and goose-type, were originally isolated from chicken and goose egg white, respectively. Chicken-type and goose-type lysozymes have similar three-dimensional structures, but different amino acid sequences (Nakano, T. and T. Graf (1991) Biochim. Biophys. Acta 1090:273-276). In chickens, both forms of lysozyme are found in neutrophil granulocytes (heterophils), but only chicken-type lysozyme is found in egg white. Generally, chicken-type lysozyme mRNA is found in both adherent monocytes and macrophages and nonadherent promyelocytes and granulocytes as well as in cells of the bone marrow, spleen, bursa, and oviduct. Goose-type lysozyme mRNA is found in non-adherent cells of the bone marrow and lung. Several isozymes have been found in rabbits, including leukocytic, gastrointestinal, and possibly lymphoepithelial forms (OMIM #153450, supra; Nakano and Graf, supra; and GenBank GI 1310929). A human lysozyme gene encoding a protein similar to chicken-type lysozyme has been cloned (Yoshimura, K. et al. (1988) Biochem. Biophys. Res. Commun. 150:794-801). A consensus motif featuring regularly spaced cysteine residues has been derived from the lysozyme C enzymes of various species (Prosite PS00128, *http://expasy.hcuge.ch* Swiss Institute of Bioinformatics). Lysozyme C shares about 40% amino acid sequence identity with α-lactalbumin.

Please replace the paragraph beginning at page 13, line 26 with the following amended paragraph:

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at *http://www.ncbi.nlm.nih.gov/BLAST/*. The BLAST software suite includes various sequence

analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at http://www.ncbi.nlm.nih.gov/gorf/bl2.html. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example: